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SEQUENCE LISTING

<110> Hageman, Gregory S.
Kuehn, Markus H.

<120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
ON A NOVEL HUMAN GENE FAMILY

<130> UIA-027.01

<140> 09/183,972

<141> 1998-10-29

<160> 49

<170> PatentIn Ver. 2.0

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<211> 555

<212> DNA

<213> Callimico sp.

<220>

<221> CDS

<222> (1)..(555)

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cag att tta gcc agt ctt caa gct tat tat aga ttg aga gtg tgt cag 96
Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln
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gaa gca gta tgg gaa gca tat cgg atc ttt ctg gat cgc atc cct gac 144
Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
35 40 45

aca ggg gaa tat cag gac tgg gtc agc ttc tgc cag cag gag acc ttc 192
Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
50 55 60

tgc ctc ttt gac atc gga caa aac ttc agc aat tcc cag gag cac ctg 240
Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
65 70 75 80

gat ctt ctc cag cag aga ata aaa cag aga agt ttc cct gag aga aaa 288
Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
85 90 95

gat gaa gta tct aca gag aag aca ttg gga gag cct agt gaa acc att 336
Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
100 105 110

gtg gtt tca aca gat gtt gcc agc gtc tca ctt ggg cct ttc cct gtc 384
Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
115 120 125



act cct gat gac acc ctc ctc aat gaa att ctc gat aat gca ctc aac 432
 Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
 130 135 140

gac acc aag atg cct aca aca gaa aga gaa aca gaa ctc gct gtg tct 480
 Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
 145 150 155 160

gag gag cag agg gtg gag ctc agc atc tct ctg ata aac cag agg ttc 528
 Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
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aag gca gag ctc gct gac tct cag tca 555
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 <213> Callimico sp.

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 35 40 45

Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
 50 55 60

Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
 65 70 75 80

Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
 85 90 95

Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
 100 105 110

Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
 115 120 125

Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
 130 135 140

Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
 145 150 155 160

Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
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Lys Ala Glu Leu Ala Asp Ser Gln Ser
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<210> 3
<211> 3261
<212> DNA
<213> Homo sapiens

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<222> (128)..(2440)

<220>
<223> "n" bases at various positions throughout the sequence
may be a, t, c, g, other or unknown

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agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile
1 5 10
C
ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat 217
Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His
15 20 25 30
tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa 265
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu
35 40 45
agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat 313
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp
50 55 60
ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt 361
Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val
65 70 75
aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa 409
Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln
80 85 90
gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat 457
Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr
95 100 105 110
cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg 505
Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp
115 120 125
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Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
130 135 140

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Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile	
145 150 155	
aaa cag aga agt ttc cct gac aga aaa gat gaa ata tct gca gag aag	649
Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys	
160 165 170	
aca ttg gga gag cct ggt gaa acc att gtc att tca aca gat gtt gcc	697
Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala	
175 180 185 190	
aac gtc tca ctt ggg cct ttc cct ctc act cct gat gac acc ctc ctc	745
Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu	
195 200 205	
aat gaa att ctc gat aat aca ctc aac gac acc aag atg cct aca aca	793
Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr	
210 215 220	
gaa aga gaa aca gaa ttc gct gtg ttg gag gag cag agg gtg gag ctc	841
Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu	
225 230 235	
agc gtc tct ctg gta aac cag aag ttc aag gca gag ctc gct gac tcc	889
Ser Val Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser	
240 245 250	
cag tcc cca tat tac cag gag cta gca gga aag tcc caa ctt cag atg	937
Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met	
255 260 265 270	
caa aag ata ttt aag aaa ctt cca gga ttc aaa aaa atc cat gtg tta	985
Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu	
275 280 285	
gga ttt aga cca aag aaa gaa aaa gat ggc tca agc tcc aca gag atg	1033
Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met	
290 295 300	
caa ctt acg gcc atc ttt aag aga cac agt gca gaa gca aaa agc cct	1081
Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro	
305 310 315	
gca agt gac ctc ctg tct ttt gat tcc aac aaa att gaa agt gag gaa	1129
Ala Ser Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu	
320 325 330	
gtc tat cat gga acc atg gag gag gac aag caa cca gaa atc tat ctc	1177
Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu	
335 340 345 350	
aca gct aca gac ctc aaa agg ctg atc agc aaa gca cta gag gaa gaa	1225
Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu	
355 360 365	

caa tct ttg gat gtg ggg aca att cag ttc act gat gaa att gct gga	1273
Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly	
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tca ctg cca gcc ttt ggt cct gac acc caa tca gag ctg ccc aca tct	1321
Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser	
385 390 395	
ttt gct gtt ata aca gag gat gct act ttg agt cca gaa ctt cct cct	1369
Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro	
400 405 410	
gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct	1417
Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro	
415 420 425 430	
gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa	1465
Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu	
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Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln	
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ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg	1609
Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu	
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Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala	
495 500 505 510	
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Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp	
515 520 525	
act cct gcc cca tct gag gta cca gag ctc agc gaa tat gtt tct gtc	1753
Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val	
530 535 540	
cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat	1801
Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr	
545 550 555	
atc acc act agt tct atg acc att gcc ccc aag ggc cga gag ctg gta	1849
Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val	
560 565 570	
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Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu	
575 580 585 590	

ttc aac aag agc tct ctg gag tac cga gct ctg gag caa caa ttc aca 1945
 Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr
 595 600 605

cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga ttt aag caa 1993
 Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln
 610 615 620

ctt gaa ata ctt aac ttc aga aac ggg agt gtg att gtg aat agc aaa 2041
 Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys
 625 630 635

atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag gct gtg cac 2089
 Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His
 640 645 650

ggg gtc ttg gag gat ttt cgt tct gct gca gcc caa caa ctc cat ctg 2137
 Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Gln Gln Leu His Leu
 655 660 665 670

C1 gaa ata gac agc tac tct ctc aac att gaa cca gct gat caa gca gat 2185
 Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp
 675 680 685

ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac 2233
 Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn
 690 695 700

gaa cgg act gag gaa gcg gag tgt cgc tgc aaa cca gga tat gac agc 2281
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 705 710 715

cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt ggc ctg gca caa 2329
 Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln
 720 725 730

agg aat gcg agg tcc tcc agg gaa agg gag ctc cat gcg gtt cca gat 2377
 Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp
 735 740 745 750

cac tct gaa aat caa gca tac aaa act agt gtt aaa agt tcc aaa atc 2425
 His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile
 755 760 765

aac aaa ata aca agg taatcagtaa aagaaattct gaattactga ccgtagaata 2480
 Asn Lys Ile Thr Arg
 770

tgaagaattt aaccatcaag attgggaagg aaattaaaaa ctgaaaatgt acaattatca 2540

cttaggctat ctcaagagag atgatttgcc ttctcaagga aaatggagac aggcatattc 2600

atgggtcatc aaaatccaga catacagtca aactgagaa tcagcacaca ccatatttca 2660

aatatagaag agtcatgtac ttggcaacca gttaaattctg aaaaaaaga cacttactta 2720

ttattaaaac cccaaatgca atcagcgaaa catattttta ctattcttgg atgatagtca 2780

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 <211> 771
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 <213> Homo sapiens

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 Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
 35 40 45
 Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
 50 55 60
 Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
 65 70 75 80
 Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
 85 90 95
 Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
 100 105 110
 Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
 115 120 125
 Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
 130 135 140
 Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
 145 150 155 160
 Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
 165 170 175

Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
 180 185 190
 Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu
 195 200 205
 Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg
 210 215 220
 Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val
 225 230 235 240
 Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser
 245 250 255
 Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys
 260 265 270
 Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe
 275 280 285
 Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu
 290 295 300
 Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser
 305 310 315 320
 Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr
 325 330 335
 His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala
 340 345 350
 Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser
 355 360 365
 Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu
 370 375 380
 Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser Phe Ala
 385 390 395 400
 Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu
 405 410 415
 Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro Asp Thr
 420 425 430
 Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu Ala Pro
 435 440 445
 Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln Gly Thr
 450 455 460
 Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly Leu Thr
 465 470 475 480

Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu Gly Ile
 485 490 495
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 Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp Thr Pro
 515 520 525
 Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
 530 535 540
 His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
 545 550 555 560
 Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe
 565 570 575
 Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu Phe Asn
 580 585 590
 Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu
 595 600 605
 Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln Leu Glu
 610 615 620
 Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys
 625 630 635 640
 Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
 645 650 655
 Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
 660 665 670
 Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
 675 680 685
 Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
 690 695 700
 Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
 705 710 715 720
 Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn
 725 730 735
 Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp His Ser
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 Ile Thr Arg
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<210> 5
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 <212> DNA
 <213> Homo sapiens

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 <221> unsure
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 <223> applicants are unsure of bases designated as "n"
 at various positions throughout the sequence

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 tgggaagtttc aaggatttgg acactcaatt aaggattctg tcctctcctc attccttttg 180
 ttttggccca a atg att atg ttt cct ctt ttt ggg aag att tct ctg ggt 230
 Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly
 1 5 10
 att ttg ata ttt gtc ctg ata gaa gga gac ttt cca tca tta aca gca 278
 Ile Leu Ile Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala
 15 20 25
 caa acc tac tta tct ata gag gag atc caa gaa ccc aag agt gca gtt 326
 Gln Thr Tyr Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val
 30 35 40 45
 tct ttt ctc ctg cct gaa gaa tca aca gac ctt tct cta gct acc aaa 374
 Ser Phe Leu Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys
 50 55 60
 aag aaa cag cct ctg gac cgc aga gaa act gaa aga cag tgg tta atc 422
 Lys Lys Gln Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile
 65 70 75
 aga agg cgg aga tct att ctg ttt cct aat gga gtg aaa atc tgc cca 470
 Arg Arg Arg Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro
 80 85 90
 gat gaa agt gtt gca gag gct gtg gca aat cat gtg aag tat ttt aaa 518
 Asp Glu Ser Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys
 95 100 105
 gtc cga gtg tgt cag gaa gct gtc tgg gaa gcc ttc agg act ttt tgg 566
 Val Arg Val Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp
 110 115 120 125
 gat cga ctt cct ggg cgt gag gaa tat cat tac tgg atg aat ttg tgt 614
 Asp Arg Leu Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys
 130 135 140

gag gat gga gtc aca agt ata ttt gaa atg ggc aca aat ttt agt gaa 662
 Glu Asp Gly Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu
 145 150 155

tct gtg gaa cat aga agc tta atc atg aag aaa ctg act tat gca aag 710
 Ser Val Glu His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys
 160 165 170

gaa act gta agc agc tct gaa ctg tct tct cca gtt cct gtt ggt gat 758
 Glu Thr Val Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp
 175 180 185

act tca aca ttg gga gac act act ctc agt gtt cca cat cca gag gtg 806
 Thr Ser Thr Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val
 190 195 200 205

gac gcc tat gaa ggt gcc tca gag agc agc ttg gaa agg cca gag gag 854
 Asp Ala Tyr Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu
 210 215 220

agt att agc aat gaa att gag aat gtg ata gaa gaa gcc aca aaa cca 902
 Ser Ile Ser Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro
 225 230 235

gca ggt gaa cag att gca gaa ttc agt atc cac ctt ttg ggg aag cag 950
 Ala Gly Glu Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln
 240 245 250

tac agg gaa gaa cta cag gat tcc tcc agc ttt cac cac cag cac ctt 998
 Tyr Arg Glu Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu
 255 260 265

gaa gaa gaa ttt att tca gag gtt gaa aat gca ttt act ggg tta cca 1046
 Glu Glu Glu Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro
 270 275 280 285

ggc tac aag gaa att cgt gta ctt gaa ttt agg tcc ccc aag gaa aat 1094
 Gly Tyr Lys Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn
 290 295 300

gac agt ggc gta gat gtt tac tat gca gtt acc ttc aat ggt gag gcc 1142
 Asp Ser Gly Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala
 305 310 315

atc agc aat acc acc tgg gac ctc att agc ctt cac tcc aac aag gtg 1190
 Ile Ser Asn Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val
 320 325 330

gaa aac cat ggc ctt gtg gaa ctg gat gat aaa ccc act gtt gtt tat 1238
 Glu Asn His Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr
 335 340 345

aca atc agt aac ttc aga gat tat att gct gag aca ttg cag cag aat 1286
 Thr Ile Ser Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn
 350 355 360 365

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 Phe Leu Leu Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln
 370 375 380

ctt atc aat gtg aga gga gtt ttg cgt cac caa act gaa gat cta gtt 1382
 Leu Ile Asn Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val
 385 390 395

tgg aac acc caa agt tca agt ctt cag gca acg ccg tca tct att ctg 1430
 Trp Asn Thr Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu
 400 405 410

gat aat acc ttt caa gct gca tgg ccc tca gca gat gaa tcc atc acc 1478
 Asp Asn Thr Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr
 415 420 425

agc agt att cca cca ctt gat ttc agc tct ggt cct ccc tca gcc act 1526
 Ser Ser Ile Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr
 430 435 440 445

ggc agg gaa ctc tgg tca gaa agt cct ttg ggt gat tta gtg tct aca 1574
 Gly Arg Glu Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr
 450 455 460

cac aaa tta gcc ttt ccc tcg aag atg ggc ctc agc tct tcc cca gag 1622
 His Lys Leu Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu
 465 470 475

gtt tta gag gtt agc agc ttg act ctt cat tct gtc acc ccg gca gtg 1670
 Val Leu Glu Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val
 480 485 490

ctt cag act ggc ttg cct gtg gct tct gag gaa agg act tct gga tct 1718
 Leu Gln Thr Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser
 495 500 505

cac ttg gta gaa gat gga tta gcc aat gtt gaa gag tca gaa gat ttt 1766
 His Leu Val Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe
 510 515 520 525

ctt tct att gat tca ttg cct tca agt tca ttc act caa cct gtg cca 1814
 Leu Ser Ile Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro
 530 535 540

aaa gaa aca ata cca tcc atg gaa gac tct gat gtg tcc tta aca tct 1862
 Lys Glu Thr Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser
 545 550 555

tca cca tat ctg acc tct tct ata cct ttt ggc ttg gac tcc ttg acc 1910
 Ser Pro Tyr Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr
 560 565 570

tcc aaa gtc aaa gac caa tta aaa gtg agc cct ttc ctg cca gat gca 1958
 Ser Lys Val Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala
 575 580 585

tcc atg gaa aaa gag tta ata ttt gac ggt ggt tta ggt tca ggg tct 2006
 Ser Met Glu Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser
 590 595 600 605

ggg caa aag gta gat ctg att act tgg cca tgg agt gag act tca tca 2054
 Gly Gln Lys Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser
 610 615 620

gag aag agc gcc gaa cca ctg tcc aag ccg tgg ctt gaa gat gat gat 2102
 Glu Lys Ser Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Asp
 625 630 635

tca ctt ttg cca gct gag att gaa gac aag aaa cta gtt tta gtt gac 2150
 Ser Leu Leu Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp
 640 645 650

aaa atg gat tcc aca gac caa att agt aag cac tca aaa tat gaa cat 2198
 Lys Met Asp Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His
 655 660 665

gat gac aga tcc aca cac ttt cca gag gaa gag cct ctt agt ggg cct 2246
 Asp Asp Arg Ser Thr His Phe Pro Glu Glu Glu Pro Leu Ser Gly Pro
 670 675 680 685

gct gtg ccc atc ttc gca gat act gca gct gaa tct gcg tct cta acc 2294
 Ala Val Pro Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr
 690 695 700

ctc ccc aag cac ata tca gaa gta cct ggt gtt gat gat tgc tca gtt 2342
 Leu Pro Lys His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val
 705 710 715

acc aaa gca cct ctt ata ctg aca tct gta gca atc tct gcc tct act 2390
 Thr Lys Ala Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr
 720 725 730

gat aaa tca gat cag gca gat gcc atc cta agg gag gat atg gaa caa 2438
 Asp Lys Ser Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln
 735 740 745

att act gag tca tcc aac tat gaa tgg ttt gac agt gag gtt tca atg 2486
 Ile Thr Glu Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met
 750 755 760 765

gta aag cca gat atg caa act ttg tgg act ata ttg cca gaa tca gag 2534
 Val Lys Pro Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu
 770 775 780

aga gtt tgg aca aga act tct tcc cta gag aaa ttg tcc aga gac ata 2582
 Arg Val Trp Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile
 785 790 795

ttg gca agt aca cca cag agt gct gac agg ctc tgg tta tct gtg aca 2630
 Leu Ala Ser Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr
 800 805 810

cag tct acc aaa ttg cct cca acc aca atc tcc acc ctg cta gag gat 2678
 Gln Ser Thr Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp
 815 820 825

gaa gta att atg ggt gta cag gat att tcg tta gaa ctg gac cgg ata 2726
 Glu Val Ile Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile
 830 835 840 845

ggc aca gat tac tat cag cct gag caa gtc caa gag caa aat ggc aag 2774
 Gly Thr Asp Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys
 850 855 860

gtt ggt agt tat gtg gaa atg tca aca agt gtt cac tcc aca gag atg 2822
 Val Gly Ser Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met
 865 870 875

gtt agt gtg gct tgg ccc aca gaa gga gga gat gac ttg agt tat acc 2870
 Val Ser Val Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr
 880 885 890

cag act tca gga gct ttg gtg gtt ttc ttc agc ctc cga gtg act aac 2918
 Gln Thr Ser Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn
 895 900 905

atg atg ttt tca gaa gat ctg ttt aat aaa aac tcc ttg gag tat aaa 2966
 Met Met Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys
 910 915 920 925

gcc ctg gag caa aga ttc tta gaa ttg ctg gtt ccc tat ctc cag tca 3014
 Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser
 930 935 940

aat ctc acg ggg ttc cag aac tta gaa atc ctc aac ttc aga aat ggc 3062
 Asn Leu Thr Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly
 945 950 955

agc att gtg gtg aac agt cga atg aag ttt gcc aat tct gtc cct cct 3110
 Ser Ile Val Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro
 960 965 970

aac gtc aac aat gcg gtg tac atg att ctg gaa gac ttt tgt acc act 3158
 Asn Val Asn Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr
 975 980 985

gcc tac aat acc atg aac ttg gct att gat aaa tac tct ctt gat gtg 3206
 Ala Tyr Asn Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val
 990 995 1000 1005

gaa tca ggt gat gaa gcc aac cct tgc aag ttt cag gcc tgt aat gaa 3254
 Glu Ser Gly Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu
 1010 1015 1020

ttt tca gag tgt ctg gtc aac ccc tgg agt gga gaa gca aag tgc aga 3302
 Phe Ser Glu Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg
 1025 1030 1035

tgc ttc cct gga tac ctg agt gtg gaa gaa cgg ccc tgt cag agt ctc 3350
 Cys Phe Pro Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu
 1040 1045 1050

tgt gac cta cag cct gac ttc tgc ttg aat gat gga aag tgt gac att 3398
 Cys Asp Leu Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile
 1055 1060 1065

atg cct ggg cac ggg gcc att tgt agg tgc cgg gtg ggt gag aac tgg 3446
 Met Pro Gly His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp
 1070 1075 1080 1085

tgg tac cga ggc aag cac tgt gag gaa ttt gtg tct gag ccc gtg atc 3494
 Trp Tyr Arg Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile
 1090 1095 1100

ata ggc atc act att gcc tcc gtg gtt gga ctt ctt gtc atc ttt tct 3542
 Ile Gly Ile Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser
 1105 1110 1115

gct atc atc tac ttc ttc atc agg act ctt caa gca cac cat gac agg 3590
 Ala Ile Ile Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg
 1120 1125 1130

agt gaa aga gag agt ccc ttc agt ggc tcc agc agg cag cct gac agc 3638
 Ser Glu Arg Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser
 1135 1140 1145

ctc tca tct att gag aat gct gtg aag tac aac ccc gtg tat gaa agt 3686
 Leu Ser Ser Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser
 1150 1155 1160 1165

cac agg gct gga tgt gag aag tat gag gga ccc tat cct cag cat ccc 3734
 His Arg Ala Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro
 1170 1175 1180

ttc tac agc tct gct agc gga gac gtg att ggt ggg ctg agc aga gaa 3782
 Phe Tyr Ser Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu
 1185 1190 1195

gaa atc aga cag atg tat gag agc agt gag ctt tcc aga gag gaa att 3830
 Glu Ile Arg Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile
 1200 1205 1210

caa gag aga atg aga gtt ttg gaa ctg tat gcc aat gat cct gag ttt 3878
 Gln Glu Arg Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe
 1215 1220 1225

gca gct ttt gtg aga gag caa caa gtg gaa gag gtt taacccaaaac 3924
 Ala Ala Phe Val Arg Glu Gln Gln Val Glu Glu Val
 1230 1235 1240

tcctgttctg aaactgatta gaagcctgga gaagatggag attacttggt acttatgtca 3984

tataattaac ctggatttta aacactgttg gaagaagagn tttctatgaa aaaattaaat 4044

atagggcaca ctgttttttt ttcagcttaa gntttcagaa tgtagtnaga gatgtwmcac 4104

ttttatttct ataaagactg aatgctgtgt ttaaataatt gaaaactacg ttaaaaaaaaa 4164

a

4165

<210> 6

<211> 1241

<212> PRT

<213> Homo sapiens

<400> 6

Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
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Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
20 25 30

Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
35 40 45

Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
50 55 60

Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
65 70 75 80

Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
85 90 95

Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
100 105 110

Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
115 120 125

Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
130 135 140

Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
145 150 155 160

His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
165 170 175

Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
180 185 190

Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
195 200 205

Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
210 215 220

Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
225 230 235 240

Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
245 250 255

Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
 260 265 270
 Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
 275 280 285
 Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
 290 295 300
 Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
 305 310 315 320
 Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
 325 330 335
 Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
 340 345 350
 Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
 355 360 365
 Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
 370 375 380
 Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
 385 390 395 400
 Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Asp Asn Thr
 405 410 415
 Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile
 420 425 430
 Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu
 435 440 445
 Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu
 450 455 460
 Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu
 465 470 475 480
 Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr
 485 490 495
 Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val
 500 505 510
 Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile
 515 520 525
 Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr
 530 535 540
 Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr
 545 550 555 560

Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val
 565 570 575
 Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala Ser Met Glu
 580 585 590
 Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser Gly Gln Lys
 595 600 605
 Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser Glu Lys Ser
 610 615 620
 Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Asp Ser Leu Leu
 625 630 635 640
 Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp Lys Met Asp
 645 650 655
 Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His Asp Asp Arg
 660 665 670
 Ser Thr His Phe Pro Glu Glu Glu Pro Leu Ser Gly Pro Ala Val Pro
 675 680 685
 Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr Leu Pro Lys
 690 695 700
 His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val Thr Lys Ala
 705 710 715 720
 Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr Asp Lys Ser
 725 730 735
 Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln Ile Thr Glu
 740 745 750
 Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met Val Lys Pro
 755 760 765
 Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu Arg Val Trp
 770 775 780
 Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile Leu Ala Ser
 785 790 795 800
 Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr Gln Ser Thr
 805 810 815
 Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp Glu Val Ile
 820 825 830
 Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile Gly Thr Asp
 835 840 845
 Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys Val Gly Ser
 850 855 860

Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met Val Ser Val
 865 870 875 880
 Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr Gln Thr Ser
 885 890 895
 Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn Met Met Phe
 900 905 910
 Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys Ala Leu Glu
 915 920 925
 Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser Asn Leu Thr
 930 935 940
 Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Ile Val
 945 950 955 960
 Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro Asn Val Asn
 965 970 975
 Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr Ala Tyr Asn
 980 985 990
 Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val Glu Ser Gly
 995 1000 1005
 Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu Phe Ser Glu
 1010 1015 1020
 Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg Cys Phe Pro
 1025 1030 1035 1040
 Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu Cys Asp Leu
 1045 1050 1055
 Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile Met Pro Gly
 1060 1065 1070
 His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp Trp Tyr Arg
 1075 1080 1085
 Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile Ile Gly Ile
 1090 1095 1100
 Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile
 1105 1110 1115 1120
 Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg
 1125 1130 1135
 Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser
 1140 1145 1150
 Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala
 1155 1160 1165

Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser
 1170 1175 1180

Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
 185 1190 1195 1200

Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
 1205 1210 1215

Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
 1220 1225 1230

Val Arg Glu Gln Gln Val Glu Glu Val
 1235 1240

<210> 7
 <211> 20
 <212> PRT
 <213> Rattus sp.

<400> 7
 Ser Ile Leu Phe Pro Asn Gly Val Arg Ile Cys Pro Ser Asp Thr Val
 1 5 10 15

Ala Glu Ala Val
 20

<210> 8
 <211> 20
 <212> PRT
 <213> Porcine sp.

<220>
 <221> MOD_RES
 <222> (1)
 <223> any, other or unknown amino acid

<220>
 <221> MOD_RES
 <222> (11)
 <223> any, other or unknown amino acid

<400> 8
 Xaa Val Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
 1 5 10 15

Lys Gln Ile Leu
 20

<210> 9
 <211> 10
 <212> PRT
 <213> Porcine sp.

<220>

<221> MOD_RES
 <222> (1)
 <223> any, other or unknown amino acid

<400> 9
 Xaa Val Leu Phe Pro Asn Gly Val Lys Ile
 1 5 10

<210> 10
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (25)
 <223> i

<400> 10
 tattaggaat tccatytyt tyccnaaygg

30

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> modified_base
 <222> (1)..(26)
 <223> "n" at positions 3, 6, 9 & 24 represent "inosine"

<400> 11
 ttncngcna gytcytrta rtangg

26

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12
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22

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

acgggggtta aagtctgtcc

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

cgaacaaaaa gatccgcatt

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

ccttctgcct ctttgacatt g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

atcaggactg ggtcagcatc

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17

tcaacagatg ttgccaacgt

20

<210> 18

<211> 20

<212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18
 gagcctgggtg aaaccattgt

20

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19
 gtggagctca gcgtctctct

20

<210> 20
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20
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19

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21
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20

<210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22
 gaaacttcca ggattcaaaa aa

22

<210> 23
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer

<400> 23
 aggaggacaa gcaaccagaa 20

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 24
 tccaacaaaa ttgaaagtga gg 22

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 25
 aatcagagct gcccacatct 20

<210> 26
 <211> 19
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer

<400> 26
 agccttttgt cctgacacc 19

<210> 27
 <211> 21
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: primer

<400> 27
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<210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 28
 agtgcagggtg gcgaagatat

20

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 29
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20

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30
 ccacctgcat cttcagatga ca

22

<210> 31
 <211> 20
 <212> DNA
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<220>

<223> Description of Artificial Sequence: primer

<400> 31
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20

<210> 32
 <211> 22
 <212> DNA
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<220>

<223> Description of Artificial Sequence: primer

<400> 32
aggataccac tcctgtctca gc

22

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
aacaattcac acagctgctg g

21

<210> 34
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
ccgagctctg gagcaac

17

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
gaggattttc gttctgctgc

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 36
tctgtgccgt ataacctcac

20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 37

gactgaggaa gcggagtgtc

20

<210> 38

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38

acgaacggac tgaggaag

18

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

ttctgaatta ctgaccgtag aa

22

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

ttccaaaatc aacaaaataa ca

22

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

ggtcacaaa atccagacat a

21

<210> 42

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 42

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27

<210> 43

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<210> 46

<211> 15

<212> PRT

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<223> any, other or unknown amino acid

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<400> 46
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 1 5 10 15

<210> 47
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 <212> PRT
 <213> Callimico sp.

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Lys Glu Ile

<210> 48
 <211> 20
 <212> PRT
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<400> 48
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Lys Gln Ile Leu
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<210> 49
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 <213> Callimico sp.

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<223> any, other or unknown amino acid

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<222> (11)

<223> any, other or unknown amino acid

<400> 49

Xaa Ile Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
1 5 10 15

Lys Gln

